

**Query=** SEQ ID NO:1  
(618 letters)

Sequences producing significant alignments:	Score (bits)	E Value
AC114490.2.1.152428	<u>1222</u>	0.0

```
>AC114490.2.1.152428
      Length = 152428
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Score = 1222 bits (616), Expect = 0.0  
Identities = 617/618 (99%)  
Strand = Plus / Minus

Query: 1 atgggggctgcctttgtcgctagcctccgcagtaaccttttcttctgccacttcaagggtca 60  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Sbjct: 107249 atgggggctgcctttgtcgctagcctccgcagtaaccttttcttctgccacttcaagggtca 107190

```
Query: 61      gagatgaacagcagtgttggggacctgggtgttggcggctgcagcctctgggatgaccct 120
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Sbjct: 107189 gagatgaacagcagtgttggggacctgggtgttggcggctgcagcctctgggatgaccct 107130
```

```
Query: 121      gctcgcttcacgtggtgcccgcgccctatgccttggcactgggcctggggctgccagcc 180
               ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 107129   gctcgcttcacgtggtgcccgcgccctatgccttggcactgggcctggggctgccagcc 107070
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Query: 181 aacgtggcggccctggcaatgttcatccgcagcggcgggcgcttggggccaggccctgctt 240  
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 Sbjct: 107069 aacgtggcggccctggcaatgttcatccgcagcggcgggcgcttggggccaggccctgctt 107010

Query: 241 ctctacctgttcaacctggctctggtgatgagttcttcacgctcacgctgcagctgtgg 300  
 |||  
 Sbjct: 107009 ctctacctgttcaacctggctctggtgatgagttcttcacgctcacgctgcagctgtgg 106950

Query: 301 ctcacctactacctgggcctggcccgaggccgcctgccacgcggccggggccacctact 360  
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 Sbjct: 106949 ctcacctactacctgggcctggcccgaggccgcctgccacgcggccggggccacctact 106890

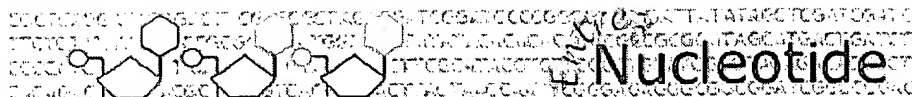
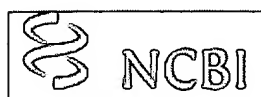
Query: 361 acgtgtccacctatgcggcggtggtcttcgccgcgctcatcagcgtgtgccgctgcggct 420  
 Sbjct: 106889 acgtgtccacctatgcggcggtggtcttcgccgcgctcatcagcgtgtgccgctgcggct 106830

Query: 421      tcgtacgcggtcccgggccaggcggtgccgcctggcccggtgcctacggbgccccg 480  
 |||  
 Spict: 106829    tcgtacgcggtcccgggccaggcggtgccgcctggcccggtgcctacggcgccccg 106770

Query: 481 cgcgcgctgcctgcgccttcgcctggctggcgggcctggccccctccctgcctggagcacc 540  
|||||  
Sbjct: 106769 cgcgcgctgcctgcgccttcgcctggctggcgggcctggccccctccctgcctggagcacc 106710

Query: 541 gctgggcaagctcggggctggcctccgccacggtggccttcgcggccgccttcctgctgg 600  
|||||  
Sbjct: 106709 gctgggcaagctcggggctggcctccgccacggtggccttcgcggccgccttcctgctgg 106650

Query: 601 tgctcgcggccaacgtga 618  
|||||  
Sbjct: 106649 tgctcgcggccaacgtga 106632



PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

Boo

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☐ 1: AC114490. Homo sapiens chro...[gi:20340495]

Links

LOCUS AC114490 152428 bp DNA linear PRI 30-APR-2002  
 DEFINITION Homo sapiens chromosome 1 clone RP11-244H3, complete sequence.  
 ACCESSION AC114490 AL354876  
 VERSION AC114490.2 GI:20340495  
 KEYWORDS HTG.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 152428)  
 AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,  
 Saenphimmachak,C., Phelps,K.A., Buckley,D., Raymond,C. and  
 Haugen,E.D.  
 TITLE Direct Submission  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 152428)  
 AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-MAR-2002) Genome Center, University of Washington,  
 Box 352145, Seattle, WA 98195, USA  
 REFERENCE 3 (bases 1 to 152428)  
 AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,  
 Saenphimmachak,C., Phelps,K.A., Buckley,D., Raymond,C. and  
 Haugen,E.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (30-APR-2002) Genome Center, University of Washington,  
 Box 352145, Seattle, WA 98195, USA  
 COMMENT On Apr 30, 2002 this sequence version replaced gi:19310309.  
 ----- Genome Center  
 Center: University of Washington Genome Center  
 Center Code: UWGC  
 Web site: <http://www.genome.washington.edu>  
 Contact: uwgchtgs@u.washington.edu  
 Drafting Center: SC  
 ----- Project Information  
 Center project name: chr-1  
 Center clone name: RP11-244H3 (sc0659)  
 ----- Summary Statistics  
 Sequencing vector: plasmid; 31% of reads  
 Sequencing vector: plasmid; L08752; 69% of reads  
 Chemistry: Dye-terminator ET; 89% of reads  
 Chemistry: Dye-terminator Big Dye; 11% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 152402 bases at least Q40  
 Consensus quality: 152428 bases at least Q30  
 Consensus quality: 152428 bases at least Q20  
 Insert size: 152428; sum-of-contigs